



SEQUENCE LISTING

<110> ~~Prayaga, Suhhirdas K
Shimkets, Richard A~~

<120> Novel Polypeptides and Polynucleotides Encoding Same

<130> 15966-615

<140> 09/732,436
<141> 2000-12-07

<150> 60/169,887
<151> 1999-12-09

<150> 60/170,230
<151> 1999-12-10

<160> 26

<170> PatentIn Ver. 2.1

<210> 1

<211> 475

<212> DNA

<213> Homo sapiens

<400> 1

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cagccttctt ttacacaagg gcttgtctga tgcttggaat agggccttcc tggacaaact 180
ccagactgga tttcatcagc agctggaaga cctggagacc tgcttggta tagaggatgg 240
gaagcaagag tctgcccctgg aaattgaggg ccctacactg gccataaaaga ggtacttcca 300
gggagttacat ttcttcttga aagagaggaa attcaggaac tgtacctggg aggttgcgt 360
aatggtaaag ggattttct taagcacaata acttcaagaaa aaagagaaca gaagaaaaga 420
gaactgcaaaa aaaaatctgg aaaaggtaat ctattnagca gaagagtgaa agctg 475

<210> 2

<211> 154

<212> PRT

<213> Homo sapiens

<400> 2

Met Val Ser Leu Leu Val Ala Leu Val Met Ile Ser Cys His Ile Tyr
1 5 . 10 15

Ser Leu Phe Cys Asp Leu Pro Lys Ala Gln Val Ile Ser Ala Leu His
20 25 30

Lys Met His Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser
35 40 45

Asp Ala Trp Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His
50 55 60

Gln Gln Leu Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys

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MIG 2 8 2002
1600/2900

AUG 28 2002
INTER 101

AUG 28 2002
INTER 101

65 70 75 80

Gln Glu Ser Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg
85 90 95

Tyr Phe Gln Gly Val His Phe Phe Leu Lys Glu Arg Lys Phe Arg Asn
100 105 110

Cys Thr Trp Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr
115 120 125

Lys Leu Gln Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn
130 135 140

Leu Glu Lys Val Ile Tyr Leu Ala Glu Glu
145 150

<210> 3

<211> 610

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (74)..(208)

<223> Wherein n is a or t or c or g.

<400> 3

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nnnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn 180
nnnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnaa agtcaggtg atttctgccc tccataagat 240
gcaccagcag atcttcagcc tcttttaca caaggcctg tctgatgctt ggaatagggc 300
cttcctggac aaactccaga ctggattca tcagcagctg gaagacctgg agacctgctt 360
tggatagag gatgggaagc aagagtctgc cctggaaattt gaggggcccta cactggccat 420
aaagaggtac ttccagggag tacatttctt cttgaaagag aggaaattca ggaactgtac 480
ctgggaggtt gtcgtaatgg taaagggatt tttcttaagc aaaaaacttc aagaaaaaga 540
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gtgaaaagctg 610

*Sub D
Unit*

<210> 4

<211> 199

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (24)..(68)

<223> Wherein Xaa is any amino acid.

<400> 4

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1 5 10 15

Ser Leu Phe Cys Asp Leu Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

	20	25	30
Xaa			
35	40	45	
Xaa			
50	55	60	
Xaa Xaa Xaa Xaa Lys Ala Gln Val Ile Ser Ala Leu His Lys Met His			
65	70	75	80
Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser Asp Ala Trp			
85	90	95	
Asn Arg Ala Phe Ile Asp Lys Leu Gln Thr Gly Phe His Gln Gln Leu			
100	105	110	
Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys Gln Glu Ser			
115	120	125	
Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg Tyr Phe Gln			
130	135	140	
Gly Val His Phe Phe Leu Lys Glu Arg Lys Phe Arg Asn Cys Thr Trp			
145	150	155	160
Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr Lys Leu Gln			
165	170	175	
Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn Leu Glu Lys			
180	185	190	
Val Ile Tyr Leu Ala Glu Glu			
195			

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<210> 5
<211> 1887
<212> DNA
<213> Homo sapiens
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cccgaccac tcttctcccg cctgcctctg ctgcgcaggc cccggccctc gcccgcctct 720
gcctgggtgc tggccttgg cggaaacccc ctgcactgca actgcgtactt ggtgtggctg 780
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ggtggcatct tcacctgcat tgcggccaat gcagctggcg aggccacagc tgctgtggag 1140
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gaggacagcg ccacggggct cacggccacg cggcctgtgg gctgcgccc 1560
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<210> 6
<211> 628
<212> PRT
<213> Homo sapiens

<400> 6
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Ser Ser Pro Pro Gln Ser Ala Thr Pro Ser Pro Cys Pro Arg Arg Cys
20 25 30

Arg Cys Gln Thr Gln Ser Leu Pro Leu Ser Val Leu Cys Pro Gly Ala
35 40 45

Gly Leu Leu Phe Val Pro Pro Ser Leu Asp Arg Arg Ala Ala Glu Leu
50 55 60

Arg Leu Ala Asp Asn Phe Ile Ala Ser Val Arg Arg Arg Asp Leu Ala
65 70 75 80

Asn Met Thr Gly Leu Leu His Leu Ser Leu Ser Arg Asn Thr Ile Arg
85 90 95

His Val Ala Ala Gly Ala Phe Ala Asp Leu Arg Ala Leu Arg Ala Leu
100 105 110

His Leu Asp Gly Asn Arg Leu Thr Ser Leu Gly Glu Gly Gln Leu Arg
115 120 125

Gly Leu Val Asn Leu Arg His Leu Ile Leu Ser Asn Asn Gln Leu Ala
130 135 140

Ala Leu Ala Ala Gly Ala Leu Asp Asp Cys Ala Glu Thr Leu Glu Asp
145 150 155 160

Leu Asp Leu Ser Tyr Asn Asn Leu Glu Gln Leu Pro Trp Glu Ala Leu
165 170 175

Gly Arg Leu Gly Asn Val Asn Thr Leu Gly Leu Asp His Asn Leu Leu
180 185 190

Ala Ser Val Pro Ala Gly Ala Phe Ser Arg Leu His Lys Leu Ala Arg
195 200 205

Leu Asp Met Thr Ser Asn Arg Leu Thr Thr Ile Pro Pro Asp Pro Leu
210 215 220

Phe Ser Arg Leu Pro Leu Leu Ala Arg Pro Arg Gly Ser Pro Ala Ser
225 230 235 240

Ala Leu Val Leu Ala Phe Gly Gly Asn Pro Leu His Cys Asn Cys Glu
245 250 255

Leu Val Trp Leu Arg Arg Leu Ala Arg Glu Asp Asp Leu Glu Ala Cys
260 265 270

Ala Ser Pro Pro Ala Leu Gly Gly Arg Tyr Phe Trp Ala Val Gly Glu
275 280 285

Glu Glu Phe Val Cys Glu Pro Pro Val Val Thr His Arg Ser Pro Pro
290 295 300

Leu Ala Val Pro Ala Gly Arg Pro Ala Ala Leu Arg Cys Arg Ala Val
305 310 315 320

Gly Asp Pro Glu Pro Arg Val Arg Trp Val Ser Pro Gln Gly Arg Leu
325 330 335

Leu Gly Asn Ser Ser Arg Ala Arg Ala Phe Pro Asn Gly Thr Leu Glu
340 345 350

Leu Leu Val Thr Glu Pro Gly Asp Gly Gly Ile Phe Thr Cys Ile Ala
355 360 365

Ala Asn Ala Ala Gly Glu Ala Thr Ala Ala Val Glu Leu Thr Val Gly
370 375 380

Pro Pro Pro Pro Gln Leu Ala Asn Ser Thr Ser Cys Asp Pro Pro
385 390 395 400

Arg Asp Gly Asp Pro Asp Ala Leu Thr Pro Pro Ser Ala Ala Ser Ala
405 410 415

Ser Ala Lys Val Ala Asp Thr Gly Pro Pro Thr Asp Arg Gly Val Gln
420 425 430

Val Thr Glu His Gly Ala Thr Ala Ala Leu Val Gln Trp Pro Asp Gln
435 440 445

Arg Pro Ile Pro Gly Ile Arg Met Tyr Gln Ile Gln Tyr Asn Ser Ser
450 455 460

Ala Asp Asp Ile Leu Val Tyr Arg Met Ile Pro Ala Glu Ser Arg Ser
465 470 475 480

Phe Leu Leu Thr Asp Leu Ala Ser Gly Arg Thr Tyr Asp Leu Cys Val
485 490 495

Leu Ala Val Tyr Glu Asp Ser Ala Thr Gly Leu Thr Ala Thr Arg Pro
500 505 510

Val Gly Cys Ala Arg Phe Ser Thr Glu Pro Ala Leu Arg Pro Cys Gly
515 520 525

Ala Pro His Ala Pro Phe Leu Gly Gly Thr Met Ile Ile Ala Leu Gly
530 535 540

Gly Val Ile Val Ala Ser Val Leu Val Phe Ile Phe Val Leu Leu Met
545 550 555 560

Arg Tyr Lys Val His Gly Gly Gln Pro Pro Gly Lys Ala Lys Ile Pro
565 570 575

Ala Pro Val Ser Ser Val Cys Ser Gln Thr Asn Gly Ala Leu Gly Pro
580 585 590

Thr Pro Thr Pro Ala Pro Pro Ala Pro Glu Pro Ala Ala Leu Arg Ala
595 600 605

His Thr Val Val Gln Leu Asp Cys Glu Pro Trp Gly Pro Gly His Glu
610 615 620

Pro Val Gly Pro
625

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<210> 7
<211> 802
<212> DNA
<213> Equus caballus

<400> 7
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ttttccccat ggcctccctg ccctctctct tgacgcctct ggtgggtgtac gagttatggc 180
cctgtggagc tctgggctgt gacctgcctc agaaccatc cctgggttagc aggaagaact 240
tcgtgcttct gggccaaatg agcagaatct cctccgcatt ctgtctgaag gacagaaaaag 300
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ctgcctggaa cacgaccctc ctggacgaaac tctgcacggg actccttcgg cagctggaaag 480
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gccctacact ggccgtgaag aggtacttcc gggggatcca tctctacctg aaagagaaga 600
aatacagtga ctgtgcctgg gagattgtcc gaatggaaat catgagatcc ttctttcat 660
cagcaaacct gcaaggaagg ttaagaatga aggtggaga ctgggctca ctttggaaatg 720
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tcttatttct gcttttagtct ag 802

<210> 8
<211> 195
<212> PRT

<213> Homo sapiens

<400> 8

Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr
1 5 10 15

Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu
20 25 30

Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser
35 40 45

Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
50 55 60

Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
85 90 95

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu
100 105 110

His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
115 120 125

Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg
130 135 140

Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser
145 150 155 160

Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe
165 170 175

Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu
180 185 190

Gly Ser Ser
195

<210> 9

<211> 195

<212> PRT

<213> Equus caballus

<400> 9

Met Ala Phe Ser Val Ser Ser Leu Met Ala Leu Val Val Ile Ser Ser
1 5 10 15

Ser Pro Val Ser Ser Met Ser Cys Asp Leu Pro Ala Ser Leu Asp Leu
20 25 30

Arg Lys Gln Glu Thr Leu Arg Val Leu His Gln Met Glu Thr Ile Ser
35 40 45

Pro Pro Ser Cys Leu Lys His Arg Thr Asp Phe Arg Phe Pro Gln Glu
50 55 60

Gln Leu Asp Gly Arg Gln Phe Pro Glu Ala Gln Ala Thr Ser Val Leu
65 70 75 80

Gln Glu Met Leu Gln Gln Ile Val Ser Leu Phe His Thr Glu Arg Ser
85 90 95

Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Arg Leu Leu Ala Gly Leu
100 105 110

His Gln Gln Leu Glu Asp Leu Asn Thr Cys Leu Asp Glu Gln Thr Gly
115 120 125

Glu Glu Glu Ser Ala Leu Gly Thr Val Gly Pro Thr Leu Ala Val Lys
130 135 140

Arg Tyr Phe Arg Arg Ile Arg Leu Tyr Leu Thr Glu Lys Lys Tyr Ser
145 150 155 160

Asp Cys Ala Trp Glu Ile Val Arg Val Asp Ile Met Arg Ser Phe Ser
165 170 175

Ser Ser Ala Asn Leu Gln Gly Arg Leu Gly Met Lys Asp Gly Asp Leu
180 185 190

Gly Ser Pro
195

Sub D5
<210> 10
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
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20 25 30

Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr
35 40 45

Arg Leu Glu Ala Cys Val Leu Gln Glu Val Glu Glu Gly Glu Ala Pro
50 55 60

Leu Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg Asn Tyr
65 70 75 80

Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys
85 90 95

Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser
100 105 110

Ser Thr Ala Leu Gln
115

<210> 11
<211> 194
<212> PRT
<213> Felis catus

<400> 11
Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
1 5 10 15

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
20 25 30

Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
35 40 45

Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp
50 55 60

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
65 70 75 80

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser
85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
100 105 110

Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Leu Gln Glu Val
115 120 125

Glu Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp
130 135 140

Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu
145 150 155 160

Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met
165 170 175

Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser
180 185 190

Glu Lys

<210> 12

<211> 195
<212> PRT
<213> Homo sapiens

<400> 12
Met Ala Phe Val Leu Ser Leu Leu Met Ala Leu Val Leu Val Ser Tyr
1 5 10 15

Gly Pro Gly Gly Ser Leu Gly Cys Asp Leu Ser Gln Asn His Val Leu
20 25 30

Val Gly Arg Lys Asn Leu Arg Leu Leu Asp Glu Met Arg Arg Leu Ser
35 40 45

Pro His Phe Cys Leu Gln Asp Arg Lys Asp Phe Ala Leu Pro Gln Glu
50 55 60

Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser Val Leu
65 70 75 80

His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr Glu His Ser
85 90 95

Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Pro Cys Arg Thr Gly Leu
100 105 110

His Gln Gln Leu Asp Asn Leu Asp Ala Cys Leu Gly Gln Val Met Gly
115 120 125

Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala Leu Lys
130 135 140

Arg Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys Gly Tyr Ser
145 150 155 160

Asp Cys Ala Trp Glu Thr Val Arg Leu Glu Ile Met Arg Ser Phe Ser
165 170 175

Ser Leu Ile Ser Leu Gln Glu Arg Leu Arg Met Met Asp Gly Asp Leu
180 185 190

Ser Ser Pro
195

horses
<210> 13
<211> 195
<212> PRT
<213> Equus caballus

<400> 13
Met Ala Leu Leu Pro Ser Leu Leu Thr Ala Leu Val Val Tyr Glu Leu
1 5 10 15

Trp Pro Cys Gly Ala Leu Gly Cys Asp Leu Pro Gln Asn His Ile Leu
20 25 30

Val Ser Arg Lys Asn Phe Val Leu Leu Gly Gln Met Ser Arg Ile Ser
 35 40 45

Ser Ala Ile Cys Leu Lys Asp Arg Lys Asp Phe Arg Phe Pro Gln Asp
 50 55 60

Met Ala Asp Gly Arg Gln Phe Pro Glu Ala Gln Ala Ala Ser Val Leu
 65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
 85 90 95

Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Glu Leu Cys Thr Gly Leu
 100 105 110

Leu Arg Gln Leu Glu Asp Leu Asp Thr Cys Leu Glu Gln Glu Met Gly
 115 120 125

Glu Glu Glu Ser Ala Leu Gly Thr Val Arg Pro Thr Leu Ala Val Lys
 130 135 140

Arg Tyr Phe Arg Gly Ile His Leu Tyr Leu Lys Glu Lys Lys Tyr Ser
 145 150 155 160

Asp Cys Ala Trp Glu Ile Val Arg Met Glu Ile Met Arg Ser Phe Ser
 165 170 175

Ser Ser Ala Asn Leu Gln Gly Arg Leu Arg Met Lys Asp Gly Asp Leu
 180 185 190

Gly Ser Pro
 195

but
D5
Um

<210> 14
 <211> 195
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr
 1 5 10 15

Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu
 20 25 30

Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser
 35 40 45

Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
 50 55 60

Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
 65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
 85 90 95

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu
100 105 110

His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
115 120 125

Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg
130 135 140

Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser
145 150 155 160

Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe
165 170 175

Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu
180 185 190

Gly Ser Ser
195

<210> 15

<211> 65

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Consensus
sequence

<400> 15

Ala Gln Ser Val Leu His Met Gln Gln Ile Phe Leu Phe Thr Glu Ser
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Ser Ala Ala Trp Asn Thr Leu Leu Thr Gly Leu Gln Leu Leu Cys Gln
20 25 30

Gly Glu Glu Ser Ala Leu Pro Leu Arg Tyr Phe Gln Gly Tyr Leu Lys
35 40 45

Glu Lys Lys Tyr Ser Cys Ala Trp Glu Val Arg Glu Ile Met Ser Leu
50 55 60

Gln
65

<210> 16

<211> 166

<212> PRT

<213> Homo sapiens

<400> 16

Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
1 5 10 15

Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu
 20 25 30

Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln
 35 40 45

Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
 50 55 60

Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
 65 70 75 80

Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
 85 90 95

His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr
 100 105 110

Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
 115 120 125

Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
 130 135 140

Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu
 145 150 155 160

Thr Gly Tyr Leu Arg Asn
 165

but D5 cent
 <210> 17
 <211> 165
 <212> PRT
 <213> Homo sapiens

<400> 17
 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
 1 5 10 15

Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
 20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
 35 40 45

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
 50 55 60

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
 65 70 75 80

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
 85 90 95

Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Asn

100	105	110
Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu		
115	120	125
Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg		
130	135	140
Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser		
145	150	155
Leu Arg Ser Lys Glu		
165		
<210> 18		
<211> 189		
<212> PRT		
<213> Mus musculus		
<400> 18		
Met Ala Arg Leu Cys Ala Phe Leu Met Val Leu Ala Val Met Ser Tyr		
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20	25	30
Arg Asn Lys Arg Ala Leu Thr Leu Leu Val Gln Met Arg Arg Leu Ser		
35	40	45
Pro Leu Ser Cys Leu Lys Asp Arg Lys Asp Phe Gly Phe Pro Gln Glu		
50	55	60
Lys Val Asp Ala Gln Gln Ile Lys Lys Ala Gln Ala Ile Pro Val Leu		
65	70	75
80		
Ser Glu Leu Thr Gln Gln Ile Leu Asn Ile Phe Thr Ser Lys Asp Ser		
85	90	95
Ser Ala Ala Trp Asn Ala Thr Leu Leu Asp Ser Phe Cys Asn Asp Leu		
100	105	110
His Gln Gln Leu Asn Asp Leu Gln Gly Cys Leu Met Gln Gln Val Gly		
115	120	125
Val Gln Glu Phe Pro Leu Thr Gln Glu Asp Ala Leu Leu Ala Val Arg		
130	135	140
Lys Tyr Phe His Arg Ile Thr Val Tyr Leu Arg Glu Lys Lys His Ser		
145	150	160
Pro Cys Ala Trp Glu Val Val Arg Ala Glu Val Trp Arg Ala Leu Ser		
165	170	175
Ser Ser Ala Asn Val Leu Gly Arg Leu Arg Glu Glu Lys		
180	185	

<210> 19
<211> 195
<212> PRT
<213> Antilocapra americana

<400> 19

Met Ala Gln Leu Leu Pro Leu Leu Thr Ala Leu Val Leu Cys Ser Tyr
1 5 10 15

Gly Pro Val Gly Ser Leu Gly Cys Asp Leu Pro His Asn Ser Ala Pro
20 25 30

Leu Ser Arg Lys Thr Leu Val Leu Leu Asp Gln Met Arg Arg Val Ser
35 40 45

Pro Val Leu Cys Leu Lys Asp Arg Arg Asp Phe Gln Phe Pro Arg Glu
50 55 60

Val Val Asn Gly Ser Gln Phe Gln Lys Asn Gln Thr Val Ser Val Leu
65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Asn Leu Leu His Thr Ala Arg Ser
85 90 95

Ser Ala Ala Trp Asn Asn Thr Leu Leu Glu Glu Leu His Thr Ala Leu
100 105 110

His Gln Gln Leu Gln Gly Leu Glu Thr Cys Leu Val Gln Ala Met Gly
115 120 125

Glu Glu Asp Ser Val Leu Thr Ala Asp Ser Pro Met Leu Met Leu Lys
130 135 140

Arg Tyr Phe Gln Arg Ile Arg Leu Tyr Leu Asp Glu Lys Lys His Ser
145 150 155 160

Gly Cys Ala Trp Glu Leu Val Arg Met Glu Ile Arg Arg Ala Phe Ser
165 170 175

Ser Thr Ala Asp Leu Gln Glu Ser Leu Arg Ser Lys Asp Gly Asp Leu
180 185 190

Ala Ser Ser
195

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<210> 20
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus sequence

<400> 20

Phe Pro Glu Gln Lys Leu Glu Met Gln Gln Ile Phe Phe Ser Ser Ala
1 5 10 15

Trp Asn Thr Leu Gln Gln Leu Leu Cys Gly Leu Leu Tyr Phe Arg Ile
20 25 30

Tyr Leu Glu Lys Lys Ser Cys Ala Trp Glu Val
35 40

<210> 21
<211> 184
<212> PRT
<213> Equus caballus

<400> 21
Met Ala Leu Pro Val Ser Leu Leu Met Ala Leu Val Val Leu Ser Cys
1 5 10 15

His Ser Ile Cys Ser Leu Gly Cys Asp Leu Pro His Thr His Ser Leu
20 25 30

Gly Asn Thr Arg Val Leu Met Leu Leu Gly Gln Met Arg Arg Ile Ser
35 40 45

Pro Phe Ser Cys Leu Lys Asp Arg Asn Asp Phe Gly Phe Pro Gln Glu
50 55 60

Val Phe Asp Gly Asn Gln Phe Arg Lys Pro Gln Ala Ile Ser Ala Val
65 70 75 80

His Glu Thr Ile Gln Gln Ile Phe His Leu Phe Ser Thr Asp Gly Ser
85 90 95

Ser Ala Ala Trp Asp Glu Ser Leu Leu Asp Lys Leu Tyr Thr Gly Leu
100 105 110

Tyr Gln Gln Leu Thr Glu Leu Glu Ala Cys Leu Ser Gln Glu Val Gly
115 120 125

Val Glu Glu Thr Pro Leu Met Asn Glu Asp Ser Leu Leu Ala Val Arg
130 135 140

Arg Tyr Phe Gln Arg Ile Ala Leu Tyr Leu Gln Glu Lys Lys Tyr Ser
145 150 155 160

Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Phe Ser
165 170 175

Ser Ser Thr Asn Leu Pro Gln Ser
180

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<210> 22
<211> 92
<212> PRT
<213> Artificial Sequence

<220>

<221> Description of Artificial Sequence:Consensus
sequence

<400> 22

Ser Leu Leu Ala Leu Val Ser Leu Gly Cys Asp Leu Pro His Leu Leu
1 5 10 15

Leu Gln Met Arg Cys Lys Asp Arg Asp Phe Phe Pro Gln Gly Gln Lys
20 25 30

Ala Gln Ser His Gln Gln Ile Phe Leu Phe Thr Ser Ser Ala Ala Trp
35 40 45

Asn Leu Leu Asp Leu Thr Gly Leu Gln Leu Leu Glu Cys Gln Glu Gly
50 55 60

Glu Leu Leu Arg Tyr Phe Gln Tyr Leu Glu Lys Lys Tyr Ser Cys Ala
65 70 75 80

Trp Glu Val Arg Glu Ile Met Ser Ser Thr Leu Gln
85 90

<210> 23

<211> 3144

<212> DNA

<213> Homo sapiens

<400> 23

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tcttcgatcc ggaaaatctt accggcatcc tccttagggag ggattattat tattatttt 180
ctttaatctg gaagagaaga gaacaagttg tgctttccc cccttcttct tgctaaacgc 240
catggatata actgaataag cggctcaggg atttcccgcc gtggacgtcc gaggccacca 300
tctgcctgca ttccggag ccggcggagg gtttagctcg agtctgtctc gggcgggaa 360
ggatgcgtgg ccgagccggg gagcccgggc gccccgcca gccggcctcg gtgccaccca 420
gccggggta gatgctgcct cgcccaggcg ctgagtgacc agaccatgga gaccctgctt 480
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gtctgccaga atctgtctga gtcactgggg accctgtgcc cctccaaggg gctgctctt 600
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cacatcagcc gccaggactt tgccaacatg acggggctgg tggacctgac cctgtccagg 720
aacaccatca gccacatcca gcccctttcc tttctggacc tcgagagcct ccgctccctg 780
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gcaagcggct ttggattgtctatgt 3144

<210> 24
<211> 832
<212> PRT
<213> Homo sapiens

<400> 24
Leu Glu Ser Val Ser Gly Gly Glu Gly Cys Val Ala Glu Pro Gly Ser
1 5 10 15

Pro Gly Ala Pro Arg Ser Arg Pro Arg Cys His Pro Ala Gly Gly Arg
20 25 30

Cys Cys Leu Ala Gln Ala Leu Ser Asp Gln Thr Met Glu Thr Leu Leu
35 40 45

Gly Gly Leu Leu Ala Phe Gly Met Ala Phe Ala Val Val Asp Ala Cys
50 55 60

Pro Lys Tyr Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Gly Thr Leu
65 70 75 80

Cys Pro Ser Lys Gly Leu Leu Phe Val Pro Pro Asp Ile Asp Arg Arg
85 90 95

Thr Val Glu Leu Arg Leu Gly Gly Asn Phe Ile Ile His Ile Ser Arg
100 105 110

Gln Asp Phe Ala Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser Arg

115	120	125
Asn Thr Ile Ser His Ile Gln Pro Phe Ser Phe Leu Asp Leu Glu Ser		
130	135	140
Leu Arg Ser Leu His Leu Asp Ser Asn Arg Leu Pro Ser Leu Gly Glu		
145	150	155
160		
Asp Thr Leu Arg Gly Leu Val Asn Leu Gln His Leu Ile Val Asn Asn		
165	170	175
Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala Phe Glu Asp Phe Leu Leu		
180	185	190
Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn Leu His Gly Leu Pro		
195	200	205
Trp Asp Ser Val Arg Arg Met Val Asn Leu His Gln Leu Ser Leu Asp		
210	215	220
His Asn Leu Leu Asp His Ile Ala Glu Gly Thr Phe Ala Asp Leu Gln		
225	230	235
240		
Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn Arg Leu Gln Lys Leu Pro		
245	250	255
Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala Ser Ala Leu Thr Ala Thr		
260	265	270
Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe Gly Gly Asn Pro Leu His		
275	280	285
Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg Leu Glu Arg Asp Asp Asp		
290	295	300
Leu Glu Thr Cys Gly Ser Pro Gly Gly Leu Lys Gly Arg Tyr Phe Trp		
305	310	315
320		
His Val Arg Glu Glu Glu Phe Val Cys Glu Pro Pro Leu Ile Thr Gln		
325	330	335
His Thr His Lys Leu Leu Val Leu Glu Gly Gln Ala Ala Thr Leu Lys		
340	345	350
Cys Lys Ala Ile Gly Asp Pro Ser Pro Leu Ile His Trp Val Ala Pro		
355	360	365
Asp Asp Arg Leu Val Gly Asn Ser Ser Arg Thr Ala Val Tyr Asp Asn		
370	375	380
Gly Thr Leu Asp Ile Phe Ile Thr Thr Ser Gln Asp Ser Gly Ala Phe		
385	390	395
400		
Thr Cys Ile Ala Ala Asn Ala Ala Gly Glu Ala Thr Ala Met Val Glu		
405	410	415
Val Ser Ile Val Gln Leu Pro His Leu Ser Asn Ser Thr Ser Arg Thr		

420	425	430
Ala Pro Pro Lys Ser Arg Leu Ser Asp Ile Thr Gly Ser Ser Lys Thr		
435	440	445
Ser Arg Gly Gly Gly Ser Gly Gly Glu Pro Pro Lys Ser Pro		
450	455	460
Pro Glu Arg Ala Val Leu Val Ser Glu Val Thr Thr Thr Ser Ala Leu		
465	470	475
Val Lys Trp Ser Val Ser Lys Ser Ala Pro Arg Val Lys Met Tyr Gln		
485	490	495
Leu Gln Tyr Asn Cys Ser Asp Asp Glu Val Leu Ile Tyr Arg Met Ile		
500	505	510
Pro Ala Ser Asn Lys Ala Phe Val Val Asn Asn Leu Val Ser Gly Thr		
515	520	525
Gly Tyr Asp Leu Cys Val Leu Ala Met Trp Asp Asp Thr Ala Thr Thr		
530	535	540
Leu Thr Ala Thr Asn Ile Val Gly Cys Ala Gln Phe Phe Thr Lys Ala		
545	550	555
Asp Tyr Pro Gln Cys Gln Ser Met His Ser Gln Ile Leu Gly Gly Thr		
565	570	575
Met Ile Leu Val Ile Gly Gly Ile Ile Val Ala Thr Leu Leu Val Phe		
580	585	590
Ile Val Ile Leu Met Val Arg Tyr Lys Val Cys Asn His Glu Ala Pro		
595	600	605
Ser Lys Met Ala Ala Ala Val Ser Asn Val Tyr Ser Gln Thr Asn Gly		
610	615	620
Ala Gln Pro Pro Pro Pro Ser Ser Ala Pro Ala Gly Ala Pro Pro Gln		
625	630	635
Gly Pro Pro Lys Val Val Val Arg Asn Glu Leu Leu Asp Phe Thr Ala		
645	650	655
Ser Leu Ala Arg Ala Ser Asp Ser Ser Ser Ser Ser Leu Gly Ser		
660	665	670
Gly Glu Ala Ala Gly Leu Gly Arg Ala Pro Trp Arg Ile Pro Pro Ser		
675	680	685
Ala Pro Arg Pro Lys Pro Ser Leu Asp Arg Leu Met Gly Ala Phe Ala		
690	695	700
Ser Leu Asp Leu Lys Ser Gln Arg Lys Glu Glu Leu Leu Asp Ser Arg		
705	710	715
Thr Pro Ala Gly Arg Gly Ala Gly Thr Ser Ala Arg Gly His His Ser		

	725	730	735												
Asp	Arg	Glu	Pro	Leu	Leu	Gly	Pro	Pro	Ala	Ala	Arg	Ala	Arg	Ser	Leu
				740			745						750		
Leu	Pro	Leu	Pro	Leu	Glu	Gly	Lys	Ala	Lys	Arg	Ser	His	Ser	Phe	Asp
				755			760					765			
Met	Gly	Asp	Phe	Ala	Ala	Ala	Ala	Gly	Gly	Val	Val	Pro	Gly	Gly	
				770			775				780				
Tyr	Ser	Pro	Pro	Arg	Lys	Val	Ser	Asn	Ile	Trp	Thr	Lys	Arg	Ser	Leu
				785			790			795			800		
Ser	Val	Asn	Gly	Met	Leu	Leu	Pro	Phe	Glu	Glu	Ser	Asp	Leu	Val	Gly
				805				810				815			
Ala	Arg	Gly	Thr	Phe	Gly	Ser	Ser	Glu	Trp	Val	Met	Glu	Ser	Thr	Val
				820			825				830				

<210> 25

<211> 98

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:IFAbd Domain
13-110

<400> 25

Gln	Phe	Gln	Lys	Glu	Asp	Ala	Ala	Leu	Thr	Ile	Tyr	Glu	Met	Leu	Gln
1				5				10				15			

Asn	Ile	Phe	Ala	Ile	Phe	Arg	Gln	Asp	Ser	Ser	Ser	Thr	Gly	Trp	Asn
				20				25				30			

Glu	Thr	Ile	Val	Glu	Asn	Leu	Leu	Ala	Asn	Val	Tyr	His	Gln	Ile	Asn
					35			40			45				

His	Leu	Lys	Thr	Val	Leu	Glu	Glu	Lys	Leu	Glu	Lys	Glu	Asp	Phe	Thr
				50			55			60					

Arg	Gly	Lys	Leu	Met	Ser	Ser	Leu	His	Leu	Lys	Arg	Tyr	Tyr	Gly	Arg
				65			70			75		80			

Ile	Leu	His	Tyr	Leu	Lys	Ala	Lys	Glu	Tyr	Ser	His	Cys	Ala	Trp	Thr
				85				90			95				

Ile Val

<210> 26

<211> 183

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:pfam00143
Domain 5-187

<400> 26

Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys Asn Ser Val Cys
1 5 10 15

Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg
20 25 30

Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys
35 40 45

Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly
50 55 60

Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn
65 70 75 80

Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala
85 90 95

Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln
100 105 110

Leu Thr Arg Leu Glu Ala Cys Val Leu Gln Glu Val Glu Glu Gly Glu
115 120 125

Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg
130 135 140

Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser
145 150 155 160

Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr
165 170 175

Tyr Ser Ser Thr Ala Leu Gln
180

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